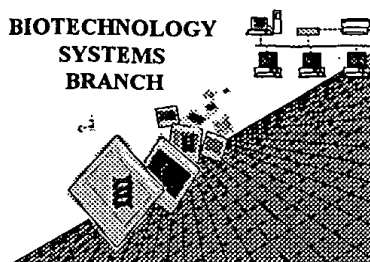


1502

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/077,712

Source:

1600 RUSH

Date Processed by STIC:

9/21/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 69/077,712
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) <u>4</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

RAW SEQUENCE LISTING

DATE: 09/21/2001

PATENT APPLICATION: US/09/077,712

TIME: 20:40:18

Input Set : A:\SEQLIST 482.1 (SCR 2025P).TXT

Output Set: N:\CRF3\09212001\I077712.raw

pp 1-2
Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Wong, Chi-Huey
5 Slee, Deborah H.
6 Laslo, Karen
8 <120> TITLE OF INVENTION: HIV Protease Inhibitors
11 <130> FILE REFERENCE: 482.1/SCR 2025P
13 <140> CURRENT APPLICATION NUMBER: US 09/077,712
14 <141> CURRENT FILING DATE: 1999-07-09
16 <150> PRIOR APPLICATION NUMBER: PCT/US96/19571
17 <151> PRIOR FILING DATE: 1996-12-09
19 <150> PRIOR APPLICATION NUMBER: US 08/568,532
20 <151> PRIOR FILING DATE: 1995-12-07
22 <160> NUMBER OF SEQ ID NOS: 7
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 8
28 <212> TYPE: PRT
29 <213> ORGANISM: Lentivirus Human Immunodeficiency virus 1
31 <400> SEQUENCE: 1
32 Ser Gln Asn Tyr Pro Ile Val Gln
33 1 5
36 <210> SEQ ID NO: 2
37 <211> LENGTH: 8
38 <212> TYPE: PRT
39 <213> ORGANISM: Lentivirus feline immunodeficiency virus
41 <400> SEQUENCE: 2
42 Pro Gln Ala Tyr Pro Ile Gln Thr
43 1 5
46 <210> SEQ ID NO: 3
47 <211> LENGTH: 6
48 <212> TYPE: PRT
49 <213> ORGANISM: Lentivirus feline immunodeficiency virus
51 <400> SEQUENCE: 3
52 Gln Ala Tyr Pro Ile Gln
53 1 5
56 <210> SEQ ID NO: 4
57 <211> LENGTH: 6
58 <212> TYPE: PRT
59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <221> NAME/KEY: MOD_RES
63 <222> LOCATION: 1
64 <223> OTHER INFORMATION: acylated with 2 amino-benzoic acid
66 <221> NAME/KEY: MOD_RES
67 <222> LOCATION: 4
68 <223> OTHER INFORMATION: para-nitro group on the phenyl ring of this
69 phenylalanine
71 <221> NAME/KEY: AMIDATION

*See item 11 on Ena Summary
Sheet*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/077,712

DATE: 09/21/2001

TIME: 20:40:18

Input Set : A:\SEQLIST 482.1 (SCR 2025P).TXT

Output Set: N:\CRF3\09212001\I077712.raw

72 <222> LOCATION: 6
 73 <223> OTHER INFORMATION: amidated with ammonia
 75 <223> OTHER INFORMATION: The first amino acid has a 2-aminobenzoic acid
 76 connected at the N-terminus.
 77 The fourth amino acid is a phenylalanine that has
 78 a para-
 W--> 79 nitro group on the ring. *max up - <2237 response has a*
 81 <400> SEQUENCE: 4 *maximum of 4 lines*
 82 Thr Ile Asn Phe Gln Arg
 83 1 5
 86 <210> SEQ ID NO: 5
 87 <211> LENGTH: 17
 88 <212> TYPE: PRT
 89 <213> ORGANISM: Unknown
 91 <220> FEATURE:
 92 <223> OTHER INFORMATION: Not listed in original publication
 94 <400> SEQUENCE: 5
 95 Gly Lys Glu Glu Gly Pro Pro Gln Ala Tyr Pro Ile Gln Thr Val Asn
 96 1 5 10 15
 97 Gly
 101 <210> SEQ ID NO: 6
 102 <211> LENGTH: 6
 103 <212> TYPE: PRT
 104 <213> ORGANISM: Artificial Sequence
 106 <220> FEATURE:
 107 <223> OTHER INFORMATION: Commercially available fluorogenic substrate for
 108 the protease of the human immunodeficiency virus
 110 <221> NAME/KEY: ACETYLATION
 111 <222> LOCATION: 1
 113 <221> NAME/KEY: MOD_RES
 114 <222> LOCATION: 4
 115 <223> OTHER INFORMATION: para-nitro group on the ring of phenylalanine
 117 <221> NAME/KEY: AMIDATION
 118 <222> LOCATION: 6
 119 <223> OTHER INFORMATION: primary amide
 121 <400> SEQUENCE: 6
 122 Thr Ile Asn Phe Gln Arg
 123 1 5
 126 <210> SEQ ID NO: 7
 127 <211> LENGTH: 8
 128 <212> TYPE: PRT
 129 <213> ORGANISM: Artificial Sequence
 131 <220> FEATURE:
 132 <221> NAME/KEY: MOD_RES
 133 <222> LOCATION: 4
 134 <223> OTHER INFORMATION: 3-amino-2-oxo-4-phenylbu-
 135 tyric acid residue
 137 <221> NAME/KEY: AMIDATION
 138 <222> LOCATION: 8

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/077,712

DATE: 09/21/2001

TIME: 20:40:18

Input Set : A:\SEQLIST 482.1 (SCR 2025P).TXT

Output Set: N:\CRF3\09212001\I077712.raw

139 <223> OTHER INFORMATION: primary amide formed with
140 ammonia
142 <223> OTHER INFORMATION: the fourth amino acid is an alpha hydroxy homolog
143 of phenyl-
144 alanine and this sequence of 8 amino acids does
145 not correspond to any known sequence
147 <400> SEQUENCE: 7
148 Pro Gln Ala Phe Pro Ile Gln Thr
149 1 5

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/077,712

DATE: 09/21/2001

TIME: 20:40:19

Input Set : A:\SEQLIST 482.1 (SCR 2025P).TXT

Output Set: N:\CRF3\09212001\I077712.raw

L:79 M:259 W: Allowed number of lines exceeded, <223> Other Information: